Listing of Claims

Claim 1 (previously presented): A method for securely storing genomic information, said method comprising obtaining genomic information of one or more individuals, separating the genomic information into more than one dataset, storing at least one such dataset in a portable storage device, and storing the remainder of the datasets in at least one central database, wherein the portable storage device is the property of the one or more individuals whose genomic information is partly contained therein, and wherein the genomic information is rendered informative only when the dataset or datasets stored in the portable storage device is combined with the dataset or datasets stored in the central database or databases.

Claim 2 (original): The method according to claim 1 wherein the information of one dataset may at least in part overlap with that of another dataset.

Claim 3 (previously presented): The method according to claim 1 wherein the information in at least one dataset may be encrypted.

Claim 4 (previously presented): The method according to claim 1 wherein the information present in one dataset that is also present in one or more other datasets is encrypted.

Claim 5 (previously presented): The method according to claim 1 wherein the information of at least one dataset is encrypted and one or more other datasets provides one or more keys for decryption.

Claim 6 (previously presented): The method according to claim 1 wherein the information of at least one dataset is encrypted and more than one encryption method is used to encrypt different parts of the information comprising the dataset(s).

Claim 7 (previously presented): The method according to claim 1 wherein said genomic information comprises nucleotide sequence information and/or annotation information.

Claim 8 (previously presented): A method for processing genomic information for secure storage wherein said genomic information comprises a representation of the nucleotide sequence of at least part of the genome of at least one individual, said method comprising converting a

nucleotide sequence into one or more fragments, representing the nucleotide sequence of one or more of said fragments by means of a unique identifier, denoting the unique identifier representing a fragment by means of a positional notation according to the position of the represented fragment in the nucleotide sequence, separating at least some of the positional notation(s) and at least some of the unique identifier(s) into at least two data sets, storing at least some of at least one dataset in a portable electronic storage device, and storing at least the remainder of the dataset(s) on at least one central database, wherein the portable storage device is the property of the one or more individuals whose genomic information is partly contained therein, and wherein the genomic information is rendered informative only when the dataset or datasets stored in the portable storage device is combined with the dataset or datasets stored in the central database or databases.

Claim 9 (original): A method for processing genomic information for secure storage wherein said genomic information comprises a representation of the nucleotide sequence of at least part of the genome of at least one individual, said method comprising converting a nucleotide sequence into one or more fragments, representing the nucleotide sequence of one or more of said fragments by means of a unique identifier, denoting the unique identifier representing a fragment by means of a positional notation according to the position of the represented fragment in the nucleotide sequence, separating at least some of the positional notation(s) and at least some of the unique identifier(s) into at least two data sets, storing at least some of at least one dataset separately from the remainder of the dataset(s), wherein access to at least some of at least one dataset may be authorised only by and/or is controlled by the one or more individuals whose genomic information is partly contained therein and/or wherein at least some of at least one dataset is the property of the one or more individuals whose genomic information is partly contained therein, and wherein the genomic information is rendered informative only when the datasets are combined.

Claim 10 (original): The method according to claim 9 wherein the representation of the sequence of nucleotides of the one or more fragments by a unique identifier is facilitated by means of a method which correlates a string of n characters of a representation of a nucleotide sequence with a unique identifier which identifies that string.

Claim 11 (original): The method according to claim 10 wherein said method utilises a lookup table.

Claim 12 (previously presented): The method according to claim 9 wherein the nucleotide sequence is converted into fragments of the same length.

Claim 13 (previously presented): The method according to claim 9 wherein the nucleotide sequence is converted into fragments of varying lengths.

Claim 14 (previously presented): The method according to claim 9 wherein the method comprises randomising the sequence of unique identifiers and their associated positional notations, and separating at least some of the positional notations from at least some of the unique identifiers whilst maintaining the association of each unique identifier with its associated positional notation.

Claim 15 (original): The method according to claim 14 wherein the association of a given unique identifier with its positional notation is maintained by their relative position within each dataset.

Claim 16 (original): The method according to claim 14 wherein the association of a given unique identifier with its positional notation is provided by a unique association identifier.

Claim 17 (previously presented): The method according to claim 9 wherein said unique identifier(s) and/or positional notation(s) and/or association identifier(s) is or are alphanumeric.

Claim 16 (original): A method for reducing the informativeness of genomic information for the secure storage of said genomic information, wherein said genomic information comprises representation information comprising a representation of the nucleotide sequence of at least part of the genome of at least one individual and/or annotation information relating to said genome, and wherein said method comprises obtaining genomic information of one or more individuals, randomising the representation of the nucleotide sequence and/or the annotation information according to a process that generates information to unrandomise said representation information and/or annotation information, and separating said representation information and/or annotation

information from the information to unrandomise said representation and/or annotation information, wherein access to at least some of said information to unrandomise said representation information and/or annotation information may be authorised only by and/or is controlled by the one or more individuals whose genomic information may thereby be unrandomised and/or wherein at least some of said information to unrandomise said representation and/or annotation information is the property of the one or more individuals whose genomic information may thereby be unrandomised, and wherein the genomnic information is rendered informative only when the representation information and/or annotation information and the information to unrandomise said representation information and/or annotation information are combined.

Claims 19 and 20 (cancelled).

Claim 21 (previously presented): A method for increasing the informativeness of stored genomic information, wherein said stored genomic information comprises or includes two or more separately stored datasets, at least one of which is stored in a portable storage device and the remainder of which are stored in at least one central database, and wherein the genomic information of any dataset(s) is uninformative in the absence of the remainder of datasets, said method comprising or including accessing said datasets, and combining the information of said datasets thereby to yield informative genomic information.

Claim 22 (original): A method for increasing the informativeness of processed genomic information wherein said processed genomic information is provided in more than one dataset, and wherein at least part of at least one such dataset comprises a randomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome, and wherein at least one other dataset comprises at least part of the information required to unrandomise at least part of said representation and/or annotation information, said method comprising or including accessing said dataset(s) comprising at least part of the information required to unrandomise at least part of said representation and/or annotation information, and unrandomising said representation and/or annotation information to yield informative genomic information.

Claim 23 (previously presented): A method for increasing the informativeness of stored genomic information, wherein said stored genomic information comprises randomised representation information comprising a randomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome(s) and information to unrandomise said representation information and/or annotation information and wherein the representation information and/or annotation information is stored separately from at least part of the information to unrandomise said representation and/or annotation information, and wherein said method comprises ~~or includes~~ accessing said information to unrandomise said representation information and/or annotation information, unrandomising the representation information and/or the annotation information using said information to unrandomise said representation information and/or annotation information to yield a unrandomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome(s).

Claim 24 (previously presented): The method according to claim 22 wherein access to at least some of said information to unrandomise said representation information and/or annotation information may be authorised only by and/or is controlled by the one or more individuals whose genomic information may thereby be unrandomised and/or wherein at least some of said information to unrandomise said representation and/or annotation information is the property of the one or more individuals whose genomic information may thereby be unrandomised.

Claim 25 (cancelled).

Claim 26 (original): Processed genomic information wherein said processed genomic information is provided in more than one dataset, and wherein at least part of at least one such dataset comprises a randomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome, and wherein at least one other dataset comprises at least part of the information required to unrandomise the representation and/or annotation information.

Claim 27 (original): The genomic information according to claim 26 wherein the dataset comprising at least part of the information required to unrandomise the representation is stored in a portable storage device.

Claim 28 (original): The genomic information according to claim 27 wherein said portable storage device is the property of the individual or individuals whose genomic information may thereby be unrandomised.

Claim 29 (cancelled).

Claim 30 (previously presented): The method according to claim 23 wherein access to at least some of said information to unrandomise said representation information and/or annotation information may be authorised only by and/or is controlled by the one or more individuals whose genomic information may thereby be unrandomised and/or wherein at least some of said information to unrandomise said representation and/or annotation information is the property of the one or more individuals whose genomic information may thereby be unrandomised.